

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/356,575

DATE: 08/02/1999  
TIME: 14:04:52

INPUT SET: S32736.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

See Item 3 on  
Error Summary  
Sheet

SEQUENCE LISTING

Does Not Comply  
Corrected Diskette Needed

(1) General Information:

(i) APPLICANT: FALLAUX et al.

(ii) TITLE OF INVENTION: PACKAGING SYSTEMS

(iii) NUMBER OF SEQUENCES: (22) 20 shown (see

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

(B) STREET: 260 SHERIDAN AVENUE, PO BOX 60039

(C) CITY: PALO ALTO

(D) STATE: CALIFORNIA

(E) COUNTRY: USA

(F) ZIP: 94306

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/793,170

(B) FILING DATE: 25-MAR-1997

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO 97/00326

(B) FILING DATE: 14-JUN-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 95201728.3

(B) FILING DATE: 26-JUN-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 95201611.1

(B) FILING DATE: 15-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: TURNER, ALLEN C.

(B) REGISTRATION NUMBER: 33,041

(C) REFERENCE/DOCKET NUMBER: 3935US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (801)532-1922

(B) TELEFAX: (801)531-9168

(C) TELEX: N/A

-->

-->

-->

move down-these  
belong  
under  
PRIOR  
APP DATA

use upper-case  
"I", not  
lower-case  
"l"

ERRORED SEQUENCES FOLLOW:

Suggestion: Consult  
Sequence Rules  
for valid format.

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40 (2) INFORMATION FOR SEQ ID NO:1: *use numeral 1* INPUT SET: S32736.raw  
41 (i) SEQUENCE CHARACTERISTICS: *hot lower-case l*  
42 (A) LENGTH: 21 base pairs  
43 (B) TYPE: nucleic acid  
44 (C) STRANDEDNESS: single  
45 (D) TOPOLOGY: linear  
46 (ii) MOLECULE TYPE: other nucleic acid *use numeral 1*  
47 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
48 DO NOT USE TAB LOSES *← more over* CGTGTAGTGT ATTTATACCC G

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49 (2) INFORMATION FOR SEQ ID NO:2:  
50 (i) SEQUENCE CHARACTERISTICS:  
51 (A) LENGTH: 21 base pairs  
52 (B) TYPE: nucleic acid  
53 (C) STRANDEDNESS: single  
54 (D) TOPOLOGY: linear  
55 (ii) MOLECULE TYPE: other nucleic acid  
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
57 TCGTCACTGG GTGGAAAGCC A *CRF program needs to "see" all bases; that is why (A) LENGTH: lines are in bold print.*

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58 (2) INFORMATION FOR SEQ ID NO:3:  
59 (i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 21 base pairs  
61 (B) TYPE: nucleic acid  
62 (C) STRANDEDNESS: single  
63 (D) TOPOLOGY: linear  
64 (ii) MOLECULE TYPE: other nucleic acid  
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
66 TACCCGCCGT CCTAAATGG C *←*

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67 (2) INFORMATION FOR SEQ ID NO:4:  
68 (i) SEQUENCE CHARACTERISTICS:  
69 (A) LENGTH: 20 base pairs  
70 (B) TYPE: nucleic acid  
71 (C) STRANDEDNESS: single  
72 (D) TOPOLOGY: linear  
73 (ii) MOLECULE TYPE: other nucleic acid  
74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
75 TGGACTTGAG CTGTAAACGC *←*

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76 (2) INFORMATION FOR SEQ ID NO:5:  
77 (i) SEQUENCE CHARACTERISTICS:  
78 (A) LENGTH: 21 base pairs  
79 (B) TYPE: nucleic acid  
80 (C) STRANDEDNESS: single  
81 (D) TOPOLOGY: linear  
82 (ii) MOLECULE TYPE: other nucleic acid  
83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
84 GCCTCCATGG AGGTCAGATG T *←*

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85 (2) INFORMATION FOR SEQ ID NO:6:  
86 (i) SEQUENCE CHARACTERISTICS:  
87 (A) LENGTH: 20 base pairs

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88          (B) TYPE: nucleic acid
89          (C) STRANDEDNESS: single
90          (D) TOPOLOGY: linear
91      (ii) MOLECULE TYPE: other nucleic acid
92          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
93                                  GCTTGAGCCC GAGACATGTC
                                  ←

94      (2) INFORMATION FOR SEQ ID NO:7:
95          (i) SEQUENCE CHARACTERISTICS:
--> 96          (A) LENGTH: 24 base pairs
97          (B) TYPE: nucleic acid
98          (C) STRANDEDNESS: single
99          (D) TOPOLOGY: linear
100      (ii) MOLECULE TYPE: other nucleic acid
101          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
102                                  CCCCTCGAGC TCAATCTGTA T
                                  ←

103      (2) INFORMATION FOR SEQ ID NO:8:
104          (i) SEQUENCE CHARACTERISTICS:
--> 105          (A) LENGTH: 27 base pairs
106          (B) TYPE: nucleic acid
107          (C) STRANDEDNESS: single
108          (D) TOPOLOGY: linear
109      (ii) MOLECULE TYPE: other nucleic acid
110          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
111                                  GGGGGATCCG AACTTGTTTA T
                                  ←

112      (2) INFORMATION FOR SEQ ID NO:9:
113          (i) SEQUENCE CHARACTERISTICS:
--> 114          (A) LENGTH: 25 base pairs
115          (B) TYPE: nucleic acid
116          (C) STRANDEDNESS: single
117          (D) TOPOLOGY: linear
118      (ii) MOLECULE TYPE: other nucleic acid
119          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
120                                  GGGAGATCTA GACATGATAA G
                                  ←

121      (2) INFORMATION FOR SEQ ID NO:10:
122          (i) SEQUENCE CHARACTERISTICS:
--> 123          (A) LENGTH: 27 base pairs
124          (B) TYPE: nucleic acid
125          (C) STRANDEDNESS: single
126          (D) TOPOLOGY: linear
127      (ii) MOLECULE TYPE: other nucleic acid
--> 128          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
129                                  GGGAGATCTG TACTGAAATG T
                                  ←

130      (2) INFORMATION FOR SEQ ID NO:11:
131          (i) SEQUENCE CHARACTERISTICS:
--> 132          (A) LENGTH: 24 base pairs
133          (B) TYPE: nucleic acid
134          (C) STRANDEDNESS: single
135          (D) TOPOLOGY: linear
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*are numbered 1*

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136 (ii) MOLECULE TYPE: other nucleic acid  
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
138 GGAGGGCTGCA GTCTCCAACG G

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--> 139 (2) INFORMATION FOR SEQ ID NO:12:  
140 (i) SEQUENCE CHARACTERISTICS:  
141 (A) LENGTH: 27 base pairs  
142 (B) TYPE: nucleic acid  
143 (C) STRANDEDNESS: single  
144 (D) TOPOLOGY: linear  
145 (ii) MOLECULE TYPE: other nucleic acid  
146 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
147 GGGGGATCCT CAAATCGTCA C

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--> 148 (2) INFORMATION FOR SEQ ID NO:13:  
149 (i) SEQUENCE CHARACTERISTICS:  
150 (A) LENGTH: 27 base pairs  
151 (B) TYPE: nucleic acid  
152 (C) STRANDEDNESS: single  
153 (D) TOPOLOGY: linear  
154 (ii) MOLECULE TYPE: other nucleic acid  
155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
156 GGGGTCTAGA CATCATCAAT A

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--> 157 (2) INFORMATION FOR SEQ ID NO:14:  
158 (i) SEQUENCE CHARACTERISTICS:  
159 (A) LENGTH: 32 base pairs  
160 (B) TYPE: nucleic acid  
161 (C) STRANDEDNESS: single  
162 (D) TOPOLOGY: linear  
163 (ii) MOLECULE TYPE: other nucleic acid  
164 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
165 GGCGAATTTCG TCGACAT

---

--> 166 (2) INFORMATION FOR SEQ ID NO:15:  
167 (i) SEQUENCE CHARACTERISTICS:  
168 (A) LENGTH: 32 base pairs  
169 (B) TYPE: nucleic acid  
170 (C) STRANDEDNESS: single  
171 (D) TOPOLOGY: linear  
172 (ii) MOLECULE TYPE: other nucleic acid  
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
174 GGCGAATTTCG GTACCAT

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--> 175 (2) INFORMATION FOR SEQ ID NO:16:  
176 (i) SEQUENCE CHARACTERISTICS:  
177 (A) LENGTH: 17 base pairs  
178 (B) TYPE: nucleic acid  
179 (C) STRANDEDNESS: single  
180 (D) TOPOLOGY: linear  
181 (ii) MOLECULE TYPE: other nucleic acid  
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
183 CTGTGTACAC CGGCGCA

09/356,575

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs *last cumulative total states 5620*
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

*more over*

TCGTAACAAC TCCGCCCCAT TGACGCAAAT GGGCGGTAGG CGTGTACGGT GGGAGGTCTA  
TGACCTCCAT AGAAGACACC GGGACCGATC CAGCCTCCGG ACTCTAGAGG ATCCGGTACT  
CGAGGAAC TG AAAAACCGA AAGTTAACTG GTAAGTTTAG TCTTTTGTG TTTTATTTCA  
CTTCTAGTAT CAAGCTTGAA TTCCTTTGTG TTACATTCTT GAATGTCGCT CGCAGTGACA  
TTAGCATTC GGTACTGTTG GTAAATGGA AGACGCCAAA AACATAAAGA AAGGCCCGGC  
GCCATTCTAT CCTCTAGAGG ATGGAACCGC TGGAGAGCAA CTGCATAAGG CTATGAAGAA  
ATACGCCCTG GTTCCTGGAA CAATTGCTTT TACAGATGCA CATATCGAGG TGAACATCAC  
GTACGCGGAA TACTTCGAAA TGTCCGTTTCG GTTGGCAGAA GCTATGAAAC GATATGGGCT  
GAATACAAAT CACAGAATCG TCGTATGCAG TGAAAACCTCT CTTCAATTCT TTATGCCGGT  
GTTGGGCGCG TTATTTATCG GAGTTGCAGT TGCGCCCGCG AACGACATTT ATAATGAACG  
TGAATTGCTC AACAGTATGA ACATTTTCGA GCCTACCGTA GTGTTTGTGTT CCAAAAAGGG  
GTTGCAAAAA ATTTTGAACG TGCAAAAAAA ATTACCAATA ATCCAGAAAA TTATTATCAT  
TGCACTGATA ATGAATTCCT CTGGATCTAC TGGGTTACCT AAGGGTGTGG CCCTTCCGCA  
TAGAACTGCC TCGGTCAGAT TCTCGCATGC CAGAGATCCT ATTTTGGCA ATCAAATCAT  
TCCGGATACT GCGATTTTAA GTGTTGTTCC ATTCCATCAC GGTTTGGAA TGTTTACTAC  
ACTCGGATAT TTGATATGTG GATTTCGAGT CGTCTTAATG TATAGATTG AAGAAGAGCT  
GTTTTTACGA TCCCTTCAGG ATTACAAAAT TCAAAGTGCG TTGCTAGTAC CAACCCTATT  
TTCATTCTTC GCCAAAAGCA CTCTGATTGA CAAATACGAT TTATCTAATT TACACGAAAT  
TGCTTCTGGG GGCGCACCTC TTTCGAAAGA AGTCGGGGAA GCGGTTGCAA AACGCTTCCA  
TCTTCCAGGG ATACGACAAG GATATGGGCT CACTGAGACT ACATCAGCTA TTCTGATTAC  
ACCCGAGGGG GATGATAAAC CGGGCGCGGT CGGTAAAGTT GTTCCATTTT TTGAAGCGAA  
GGTTGTGGAT CTGGATACCG GGAAAACGCT GGGCGTTAAT CAGAGAGGCG AATTATGTGT  
CAGAGGACCT ATGATTATGT CCGGTTATGT AAACAATCCG GAAGCGACCA ACGCCTTGAT  
TGACAAGGAT GGATGGCTAC ATTCTGGAGA CATAGCTTAC TGGGACGAAG ACGAACACTT  
CTTCATAGTT GACCGCTTGA AGTCTTTAAT TAAATACAAA GGATATCAGG TGGCCCCCGC  
TGAATTGGAA TCGATATTGT TACAACACCC CAACATCTTC GACGCGGGCG TGGCAGGTCT  
TCCCGACGAT GACGCCGGTG AACTTCCCGC CGCCGTTGTT GTTTTGGAGC ACGGAAAGAC  
GATGACGGAA AAAGAGATCG TGGATTACGT CGCCAGTCAA GTAACAACCG CGAAAAAGTT  
GCGCGGAGGA GTTGTGTTTG TGGACGAAGT ACCGAAAGGT CTTACCGGAA AACTCGACGC  
AAGAAAAATC AGAGAGATCC TCATAAAGGC CAAGAAGGGC GGAAAGTCCA AATTGTAAAA  
TGTAAC TGTA TTCAGCGATG ACGAAATTCT TAGCTATTGT AATGGGGGAT CCCCAACTTG  
TTTATTGCAG CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATTT CACAAATAAA  
GCATTTTTTT CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT ATCTTATCAT  
GTCTGGATCG GATCGATCCC CGGGTACCGA GCTCGAATTC GTAATCATGG TCATAGCTGT  
TTCTGTGTG AAATTGTTAT CCGCTCACAA TTCCACACAA CATAACGAGC GGAAGCATAA  
AGTGTAAGC CTGGGGTGCC TAATGAGTGA GCTAACTCAC ATTAATTGCG TTGCGCTCAC  
TGCCCGCTTT CCAGTCGGGA AACCTGTCGT GCCAGCTGCA TTAATGAATC GGCCAACGCG  
CGGGGAGAGG CGGTTTGCGT ATTGGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC  
GCTCGGTCGT TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT  
CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAGGCCA  
GGAACCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC  
ATCACAAAAA TCGACGCTCA AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC  
AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG  
GATACCTGTC CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCATAGC TCACGCTGTA  
GGTATCTCAG TTCGGTGTAG GTCGTTTCGT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG  
TTCAGCCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC

CTTTCCTACT  
TTGGCAGTAC  
CCCCATTGAC

TATAAGCAGA  
1080  
1140  
GGTCCCGGAT

GGATTCTAAA  
ACCTCCCGGT

*all text and cumulative base totals need to be visible on page*

ACGACTTATC GCCACTGGCA GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG  
 GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC CTAACACGG CTACACTAGA AGGACAGTAT  
 TTGGTATCTG CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT  
 CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC  
 GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT  
 GGAACGAAAA CTCACGTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT  
 AGATCCTTTT AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT  
 GGTCTGACAG TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC  
 GTTCATCCAT AGTTGCCTGA CTCCCCGTCG TGTAGATAAC TACGATACGG GAGGGCTTAC  
 CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG CTCACCGGCT CCAGATTTAT  
 CAGCAATAAA CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG TGGTCCTGCA ACTTTATCCG  
 CCTCCATCCA GTCTATTAAT TGTTTGCCGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA  
 GTTTGCGCAA CGTTGTTGCC ATTGCTACAG GCATCGTGGT GTCACGCTCG TCGTTTGTA  
 TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC CCCATGTTGT  
 GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG  
 TGTTATCACT CATGGTTATG GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA  
 GATGCTTTTC TGTGACTGGT GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC  
 GACCGAGTTG CTCTTGCCCC GCGTCAATAC GGGATAATAC CGCGCCACAT AGCAGAACTT  
 TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC  
 TGTTGAGATC CAGTTCGATG TAACCCACTC GTGCACCCAA CTGATCTTCA GCATCTTTTA  
 CTTTCACCAG CGTTTCTGGG TGAGCAAAAA CAGGAAGGCA AAATGCCGCA AAAAAGGGAA  
 TAAGGGCGAC ACGGAAATGT TGAATACTCA TACTCTTCCT TTTTCAATAT TATTGAAGCA  
 TTTATCAGGG TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC  
 AAATAGGGGT TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCTAA GAAACCATTA  
 TTATCATGAC ATTAACCTAT AAAAATAGGC GTATCACGAG GCCTATGCGG TGTGAAATAG  
 CGCACAGATG CGTAAGGAGA AAATACCGCA TCAGGCGCCA TTCGCCATTC AGGCTGCGCA  
 ACTGTTGGGA AGGGCGATCG GTGCGGGCCT CTTGCTATT ACGCCAGCTG GCGAAAGGGG  
 GATGTGCTGC AAGGCGATTA AGTTGGGTAA CGCCAGGGT TTCCAGTCA CGACGTTGTA

AAACGACGGC CAGTGCC

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

*Seqs 20 and 21 missing*

- (ii) MOLECULE TYPE: other nucleic acid
- (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTACACTGAC CTAGTGCCGC CCGGGCAAAG CC~~CGG~~CGGC ACTAG

45

*what is this? There are invalid  
 nucleic acid designations,  
 per 1.822(b) of Sequence  
 Rules.*

*Please ensure: 1) all (A) LENGTH responses reflect  
 actual number of bases  
 2) all bases are valid nucleic acid  
 designations, per 1.822(b) of Sequence  
 Rules.*